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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/029,840

DATE: 04/12/2002

TIME: 14:27:57

Input Set : A:\EP.txt

Output Set: N:\CRF3\04122002\J029840.raw

3 <110> APPLICANT: Meng, Xiang-Jin
4 Haqshenas, Gholamreza
5 Huang, Fang-Fang
7 <120> TITLE OF INVENTION: Avian Hepatitis E Virus, Vaccines and Methods of Protecting
Against Avian
8 Hepatitis-Spenomegaly Syndrome and Mammalian Hepatitis E
10 <130> FILE REFERENCE: AM100389
12 <140> CURRENT APPLICATION NUMBER: US 10/029,840
13 <141> CURRENT FILING DATE: 2001-12-31
15 <160> NUMBER OF SEQ ID NOS: 11
17 <170> SOFTWARE: PatentIn version 3.1
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 3946
21 <212> TYPE: DNA
22 <213> ORGANISM: Hepatitis E virus
24 <400> SEQUENCE: 1

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27	taccagctgg cgcaccgtat cccaccgttg cccttgggac gtttgatat ttttgcgtac	120
29	tgattatccg actatcacca caaccagtag ggtgctgcgg tctgttggtg ttaccggtag	180
31	aaccattggt cagaagatag tgtttaccca ggtggccaag cagtcgaacc cggggtccat	240
33	aacgggtccat gaggcgcagg gcagtacttt tgatcagact actataatcg ccacgttaga	300
35	tgctcgtggc cttatagctt catctcgcgc gcatgccata gttgcgctaa cccgccaccg	360
37	ggagcgtgt agtgtgattg atgttggtgg ggtgctggtc gagattggag ttactgatgc	420
39	catgtttaac aatatcgaaa tgcagcttgt gcgacctgat gctgcagccc ctgccgggt	480
41	gctacgagcc ccagacgaca ccgtggatgg cttgttggtg atacccccgg cccacactga	540
43	tgtagcggcg gtgttaacag ctgaggcgat tgggcatgcg ccccttgaat tggccgccat	600
45	aaatccaccc gggcctgtat tggagcaggg cctattatac atgccggcca ggcttgatgg	660
47	gcgtgatgag gttgttaagc tccagctgtc ggatactgta cactgcgcgc tggctgcacc	720
49	cactagccgt cttgcggtga ttaacacatt ggttgggcgg tacggtaaag ccactaagct	780
51	gcctgagggt gaatatgact taatggacac tattgcgcag ttctggcatc atatcggacc	840
53	aatcaacccc tcaacactgg agtatgcaga gatgtgcgag gccatgotta gtaagggcc	900
55	ggatgggtcc ttgattgtac atctggattt acaggatgct gattgttctc gcataacatt	960
57	cttcacagaag gactgcgcta aatttacgct ggatgacct gttgcacacg gtaaagtggg	1020
59	acaggggata tctgcgtggc cgaaaacttt gtgtgcactt ttccggccct ggttccgggc	1080
61	tatagagaag caccttgttg ctgggttacc cccaggttat tactatgggg acctgtacac	1140
63	ggaagccgat ctgcatcgtt ctgtgctttg cgcgcctgct ggtcaccttg tttttgagaa	1200
65	tgattttcca gagtttgact caacgcagaa taatgtgtcc cttgatctcg aatgtgaatt	1260
67	gatgcgcagg tttgggatgc ccgattggat ggtagccttg taccatcttg ttogatcata	1320
69	ctggctcttg gttgccccga aagaagccct tctgtgctgt tggaaaaaac actctggtga	1380
71	gccgggcacc cttttgtgga atacagtttg gaacatgact gtgttgcatc atgtttatga	1440
73	gtttgatcga ccaagtgtgt tgtgtttcaa aggtgatgat agtgtcgttg tctgtgaatc	1500
75	ggtgcgcgcc cgtccagagg gcgttagtct cgtggcagac tgcgggctaa aatgaagga	1560
77	caagaccggc ccgtgtggcg ctttttccaa cctgctgata ttcccgggag ctggtgttgt	1620
79	ctgcgacctg ttacggcagt ggggcgcgtt gactgacaag aactgggggc ccgacattca	1680

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85 tgagggtggt tggggggctt tgaaggcctg cgcgcagacc cgcgagaccc tagtgaccaa 1860
87 caggttgccg gtactaaact tatctaagga ggactgaaca aataacaatc attatgcagt 1920
89 ctgcgcgtcc atgtgcctta gctgccagtt ctgggtgttt gagtgccagg aaagtggggg 1980
91 gggatgtcgc tgtgtagatt gttgctcatg cttgcaatgt gctgcggggg gtcaaggggc 2040
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95 tggagcactc aacaacgccc cgaggagccc gtcggccccc cccctctcac agacgttgtc 2160
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109 gtgcttcagc cgggctctgc tggtttgctg actataccac atgagcgttt ggcgtataag 2580
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125 tacatgtacg gccggcctgt ggggaacgcg aacggcgagc ctgaggtgaa actgtatatg 3060
127 tcggttgagg atgcggttaa cgataaacct attatggtcc cccatgacat cgacctcggg 3120
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135 tttggggccg gcagcaccat gatggtgcat aatttgatca ctggtgtgcg cgcggccgcc 3360
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149 tgccgccagg cgccagaaga ccagtcacct gagacgcgcc ggctcctaga ccggcttagt 3780
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153 tctgggcgta attgccccta tgtttaattt attgtgattt ttataactgt tcatttgatt 3900
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158 <210> SEQ ID NO: 2

159 <211> LENGTH: 146

160 <212> TYPE: PRT

161 <213> ORGANISM: Hepatitis E virus

163 <400> SEQUENCE: 2

165 Pro Ala Leu Asp Phe Asp Gly Arg Cys Leu Thr Ser Ala Val Asp Leu

166 1 5 10 15

169 Gly Leu Gln Pro Thr Ser Trp Arg Thr Val Ser His Arg Cys Pro Trp

170 20 25 30

173 Asp Val Cys Ile Phe Leu Arg Thr Asp Tyr Pro Thr Ile Thr Thr Thr

174 35 40 45

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177 Ser Arg Val Leu Arg Ser Val Val Phe Thr Gly Glu Thr Ile Gly Gln
178      50                      55                      60
181 Lys Ile Val Phe Thr Gln Val Ala Lys Gln Ser Asn Pro Gly Ser Ile
182 65                      70                      75                      80
185 Thr Val His Glu Ala Gln Gly Ser Thr Phe Asp Gln Thr Thr Ile Ile
186                      85                      90                      95
189 Ala Thr Leu Asp Ala Arg Gly Leu Ile Ala Ser Ser Arg Ala His Ala
190                      100                      105                      110
193 Ile Val Ala Leu Thr Arg His Arg Glu Arg Cys Ser Val Ile Asp Val
194                      115                      120                      125
197 Gly Gly Val Leu Val Glu Ile Gly Val Thr Asp Ala Met Phe Asn Asn
198      130                      135                      140
201 Ile Glu
202 145
205 <210> SEQ ID NO: 3
206 <211> LENGTH: 439
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208 <213> ORGANISM: Hepatitis E virus
210 <400> SEQUENCE: 3
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215 tgattatccg actatcacca caaccagtag ggtgctgcgg tctgttgtgt ttaccggtga      180
217 aaccattggt cagaagatag tgtttaccca ggtggccaag cagtcgaacc ccgggtccat      240
219 aacgggtccat gaggcgcagg gcagtaacttt tgatcagact actataatcg ccacgttaga      300
221 tgctcgtggc cttatagctt catctcgcgc gcatgccata gttgcgctaa cccgccaccg      360
223 ggagcgctgt agtgtgattg atgttggttg ggtgctggtc gagattggag ttactgatgc      420
225 catgtttaac aatatcgaa                                     439
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229 <211> LENGTH: 483
230 <212> TYPE: PRT
231 <213> ORGANISM: Hepatitis E virus
233 <400> SEQUENCE: 4
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239 Asp Asp Thr Val Asp Gly Leu Leu Asp Ile Pro Pro Ala His Thr Asp
240                      20                      25                      30
243 Val Ala Ala Val Leu Thr Ala Glu Ala Ile Gly His Ala Pro Leu Glu
244                      35                      40                      45
247 Leu Ala Ala Ile Asn Pro Pro Gly Pro Val Leu Glu Gln Gly Leu Leu
248      50                      55                      60
251 Tyr Met Pro Ala Arg Leu Asp Gly Arg Asp Glu Val Val Lys Leu Gln
252 65                      70                      75                      80
255 Leu Ser Asp Thr Val His Cys Arg Leu Ala Ala Pro Thr Ser Arg Leu
256                      85                      90                      95
259 Ala Val Ile Asn Thr Leu Val Gly Arg Tyr Gly Lys Ala Thr Lys Leu
260                      100                      105                      110
263 Pro Glu Val Glu Tyr Asp Leu Met Asp Thr Ile Ala Gln Phe Trp His
264                      115                      120                      125
267 His Ile Gly Pro Ile Asn Pro Ser Thr Leu Glu Tyr Ala Glu Met Cys

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268      130      135      140
271 Glu Ala Met Leu Ser Lys Gly Gln Asp Gly Ser Leu Ile Val His Leu
272 145      150      155      160
275 Asp Leu Gln Asp Ala Asp Cys Ser Arg Ile Thr Phe Phe Gln Lys Asp
276      165      170      175
279 Cys Ala Lys Phe Thr Leu Asp Asp Pro Val Ala His Gly Lys Val Gly
280      180      185      190
283 Gln Gly Ile Ser Ala Trp Pro Lys Thr Leu Cys Ala Leu Phe Gly Pro
284      195      200      205
287 Trp Phe Arg Ala Ile Glu Lys His Leu Val Ala Gly Leu Pro Pro Gly
288      210      215      220
291 Tyr Tyr Tyr Gly Asp Leu Tyr Thr Glu Ala Asp Leu His Arg Ser Val
292 225      230      235      240
295 Leu Cys Ala Pro Ala Gly His Leu Val Phe Glu Asn Asp Phe Ser Glu
296      245      250      255
299 Phe Asp Ser Thr Gln Asn Asn Val Ser Leu Asp Leu Glu Cys Glu Leu
300      260      265      270
303 Met Arg Arg Phe Gly Met Pro Asp Trp Met Val Ala Leu Tyr His Leu
304      275      280      285
307 Val Arg Ser Tyr Trp Leu Leu Val Ala Pro Lys Glu Ala Leu Arg Gly
308      290      295      300
311 Cys Trp Lys Lys His Ser Gly Glu Pro Gly Thr Leu Leu Trp Asn Thr
312 305      310      315      320
315 Val Trp Asn Met Thr Val Leu His His Val Tyr Glu Phe Asp Arg Pro
316      325      330      335
319 Ser Val Leu Cys Phe Lys Gly Asp Asp Ser Val Val Val Cys Glu Ser
320      340      345      350
323 Val Arg Ala Arg Pro Glu Gly Val Ser Leu Val Ala Asp Cys Gly Leu
324      355      360      365
327 Lys Met Lys Asp Lys Thr Gly Pro Cys Gly Ala Phe Ser Asn Leu Leu
328      370      375      380
331 Ile Phe Pro Gly Ala Gly Val Val Cys Asp Leu Leu Arg Gln Trp Gly
332 385      390      395      400
335 Arg Leu Thr Asp Lys Asn Trp Gly Pro Asp Ile Gln Arg Met Gln Asp
336      405      410      415
339 Leu Glu Gln Ala Cys Lys Asp Phe Val Ala Arg Val Val Thr Gln Gly
340      420      425      430
343 Lys Glu Met Leu Thr Ile Gln Leu Val Ala Gly Tyr Tyr Gly Val Glu
344      435      440      445
347 Val Gly Met Val Glu Val Val Trp Gly Ala Leu Lys Ala Cys Ala Ala
348      450      455      460
351 Ala Arg Glu Thr Leu Val Thr Asn Arg Leu Pro Val Leu Asn Leu Ser
352 465      470      475      480
355 Lys Glu Asp
359 <210> SEQ ID NO: 5
360 <211> LENGTH: 1450
361 <212> TYPE: DNA
362 <213> ORGANISM: Hepatitis E virus
364 <400> SEQUENCE: 5

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365 gcttgtgcga cctgatgctg cagcccctgc cggggtgcta cgagccccag acgacaccgt      60
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369 ggcgattggg catgcgcccc ttgaattggc cgccataaat ccaccgggc ctgtattgga      180
371 gcagggccta ttatacatgc cggccaggct tgatgggcgt gatgaggttg ttaagctcca      240
373 gctgtcggat actgtacact gccgcctggc tgcacccact agccgtcttg cggtgattaa      300
375 cacattggtt ggcgcgtacg gtaaagccac taagctgcct gaggttgaat atgacttaat      360
377 ggacactatt gcgcagttct ggcacatat cggaaccaatc aaccctcaa cactggagta      420
379 tgcagagatg tgcgaggcca tgcttagtaa gggccaggat gggtccttga ttgtacatct      480
381 ggattttacag gatgctgatt gttctcgcat aacattcttc cagaaggact gcgctaaatt      540
383 tacgctggat gacctgttg cacacggtaa agtgggacag gggatatctg cgtggccgaa      600
385 aacttttgtt gcacttttcg gccctggtt ccgggctata gagaagcacc ttgtggctgg      660
387 gttacccccca ggttattact atggggacct gtacacggaa gccgatctgc atcgttctgt      720
389 gctttgcgcg cctgctggtc acctgtttt tgagaatgat ttctcagagt ttgactcaac      780
391 gcagaataat gtgtcccttg atctogaatg tgaattgatg cgcaggtttg ggatgcccgga      840
393 ttggatggta gccttgtaac atcttgttcg atcatactgg ctcttggttg ccccgaaaga      900
395 agcccttcgt ggctgttgga aaaaacactc tggtgagccg ggcacccttt tgtggaatac      960
397 agtttggaac atgactgtgt tgcacatgtt ttatgagttt gatcgaccaa gtgtgttgtg     1020
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405 ccgcttgact gacaagaact gggggcccga cattcagcgg atgcaggacc ttgagcaagc     1260
407 gtgtaaggat tttgttgcaac gtgttgtaac tcagggtaaa gagatgttga ccatccagct     1320
409 tgtggcgggt tattatgggt tggaagttgg tatggttgag gtggtttggg gggctttgaa     1380
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413 taaggaggac                                     1450
416 <210> SEQ ID NO: 6
417 <211> LENGTH: 606
418 <212> TYPE: PRT
419 <213> ORGANISM: Hepatitis E virus
421 <400> SEQUENCE: 6
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428          20          25          30
431 Arg Arg Asp Asn Ser Ala Gln Trp Ser Thr Gln Gln Arg Pro Glu Gly
432          35          40          45
435 Ala Val Gly Pro Ala Pro Leu Thr Asp Val Val Thr Ala Ala Gly Thr
436          50          55          60
439 Arg Thr Val Pro Asp Val Asp Gln Ala Gly Ala Val Leu Val Arg Gln
440 65          70          75          80
443 Tyr Asn Leu Val Thr Ser Pro Leu Gly Leu Ala Thr Leu Gly Ser Thr
444          85          90          95
447 Asn Ala Leu Leu Tyr Ala Ala Pro Val Ser Pro Leu Met Pro Leu Gln
448          100         105         110
451 Asp Gly Thr Thr Ser Asn Ile Met Ser Thr Glu Ser Ser Asn Tyr Ala
452          115         120         125
455 Gln Tyr Arg Val Gln Gly Leu Thr Val Arg Trp Arg Pro Val Val Pro
456          130         135         140
459 Asn Ala Val Gly Gly Phe Ser Ile Ser Met Ala Tyr Trp Pro Gln Thr

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